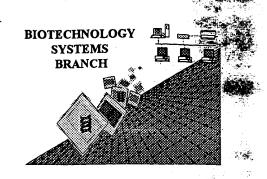# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: ___08/940,544A___

Art Unit / Team No. : ___1642___

Date Processed by STIC: ___6/22/99___

THE ATTACHED PRINTOUT EXPLAINS THE **ERRORS DETECTED.**

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: _08/940,544A_ |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or **Xaa's** (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain sourc f genetic material in <220> t <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do n t us "C py t Disk" function f PatentIn v rsion 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

J, Burke

> This Raw Listing contains the General Information
> Section and up to first 5 pages.

Does Not Comply
Corrected Diskette Needed

See item 13 on Err summary sheet for explanation of missing mandatory item

E-->	1	<110>
E-->	2	<120>
W-->	3	<130>
	4	<140> US/08/940,544A
	5	<141> 1997-09-30
	6	<160> 4
	7	<170> PatentIn Ver. 2.0
	8	<210> 1
	9	<211> 27
	10	<212> DNA
	11	<213> HUMAN
	12	<220>
	13	<223> Upstream primer for PCR amplification.
	14	<400> 1
	15	gcggccgcaa ttgaagttat gtatcct 27
	16	<210> 2
	17	<211> 30
	18	<212> DNA
	19	<213> HUMAN
	20	<220>
	21	<223> Downstream primer for PCR amplification.
	22	<400> 2
	23	tcgaggatct tgtcaggagc gataggctgc 30
	24	<210> 3
	25	<211> 717
	26	<212> DNA
	27	<213> HUMAN
	28	<220>
	29	<223> 5F11-scFv
	30	<220>
	31	<221> unsure
	32	<222> (37)
	33	<220>
	34	<221> unsure
	35	<222> (79)
	36	<400> 3
W-->	37	caggtgaaac tgcagcagtc aggacctgaa ctggtgnagc ctggggcttc agtgaagata 60
W-->	38	tcctgcaaga cttctggana caaattcact gaatacacca tgcactgggt gaagcagagc 120
	39	catggaaaga gccttgagtg gattggaggt attaatccta caatggtgg tactaactac 180
	40	aagcagaagt tcaagggcaa ggccacattg actgtagaca agtcctccag cacagcctac 240
	41	atggagctcc gcagcctgac atctgaggat tctgcagtct attactgtgc aagagatact 300
	42	acggtcccgt ttgcttactg ggtccaaggg accacggtca ccgtctcctc aggtggaggc 360

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43        ggttcaggcg gaggtggctc tggcggtggc ggatcggaca tcgagctcac tcagtctcca 420
44        gcaatcatgt ctgcatctcc aggggagaag gtcaccatga cctgcagtgg cagctcaagt 480
45        ataagttaca tgcactggta ccagcagaag cctgtcacct cccccaaaag atggatttat 540
46        gacacatcca aactggcttc tggagtccct gctcgcttca gtggcagtgg gtctgggacc 600
47        tcttattctc tcacaatcag cagcatggag gctgtagatg ctgccactta ttactgccat 660
48        cagcggagta gttacccgct cacgttcggt gctgggacac agttggaaat aaaacgg    717
49   <210> 4
50   <211> 714
51   <212> DNA
52   <213> HUMAN
53   <220>
54   <223> 3G6-scFv
55   <400> 4
56        agtattgtga tgacccagac tcccaaattc ctgcttgtat cagcaggaga cagggttacc 60
57        ataacctgca aggccagtca gagtgtgagt aatgatgtgg cttggtacca acagaagcca 120
58        gggcagtctc cgaaactgct gatatactct gcatccaatc gctacactgg agtccctgat 180
59        cgcttcactg gcagtggata tgggacggat ttcactttca ccatcagcac tgtgcaggct 240
60        gaagacctgg cagtttattt ctgtcagcag gattatagct cgctcggagg ggggaccaag 300
61        ctggaaataa aaggtggagg cggttcaggc ggaggtggct ctggcggtgg cggatcgcag 360
62        gtgcaggtga aggagtcagg acctggcctg gtggcgccct cacagagcct gtccatcact 420
63        tgcactgtct ctgggttttc attaaccaat tatggtgtac actgggttcg ccagcctcca 480
64        ggaaagggtc tggagtggct gggagtaata tgggctggtg aagcacaaa ttataattcg 540
65        gctcttatgt ccagactgag catcagcaag acaactcca agagccaagt tttcttaaaa 600
66        atgaacagtc tgcaaactga tgacacagcc atgtactact gtgccagtcg ggggggtaac 660
67        tacggctatg ctttggacta ctggggtcaa ggaacctcag tcaccgtctc ctca    714
```

Line ? Error/Warning   Original Text
----- - ------------------------------------- ---
    1 E Response to "Applicant" Name is Missing
    2 E Response to "Title of Invention" Missing
    3 W Response to "File Reference" is Missing
   37 W "N" or "Xaa" used: Feature required   caggtgaaac tgcagcagtc aggacctgaa ctggtgna
   38 W "N" or "Xaa" used: Feature required   tcctgcaaga cttctggana caaattcact gaatacac